

FIG. 1A

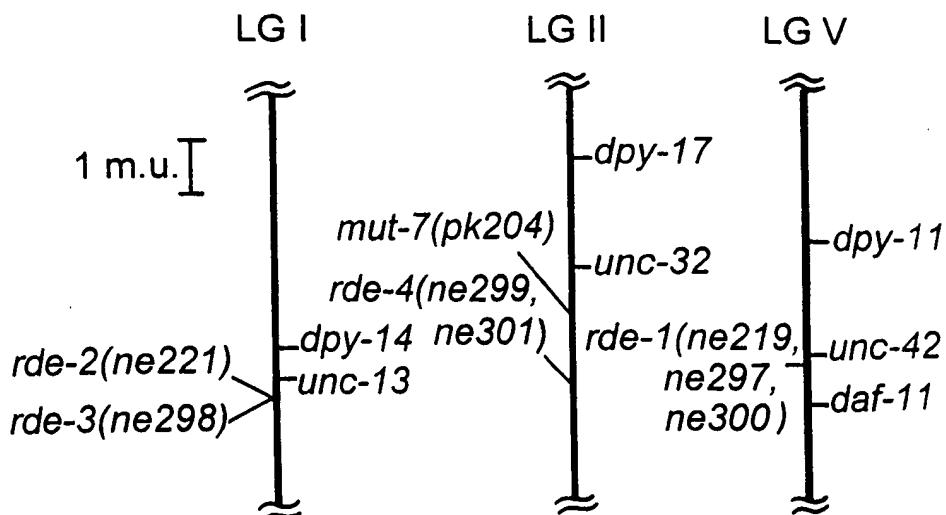


FIG. 1B

BEST AVAILABLE COPY

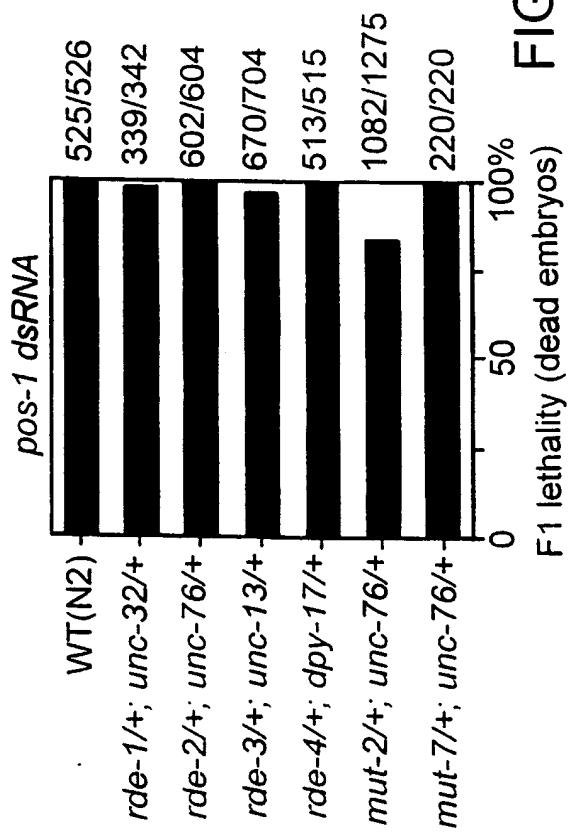


FIG. 2A

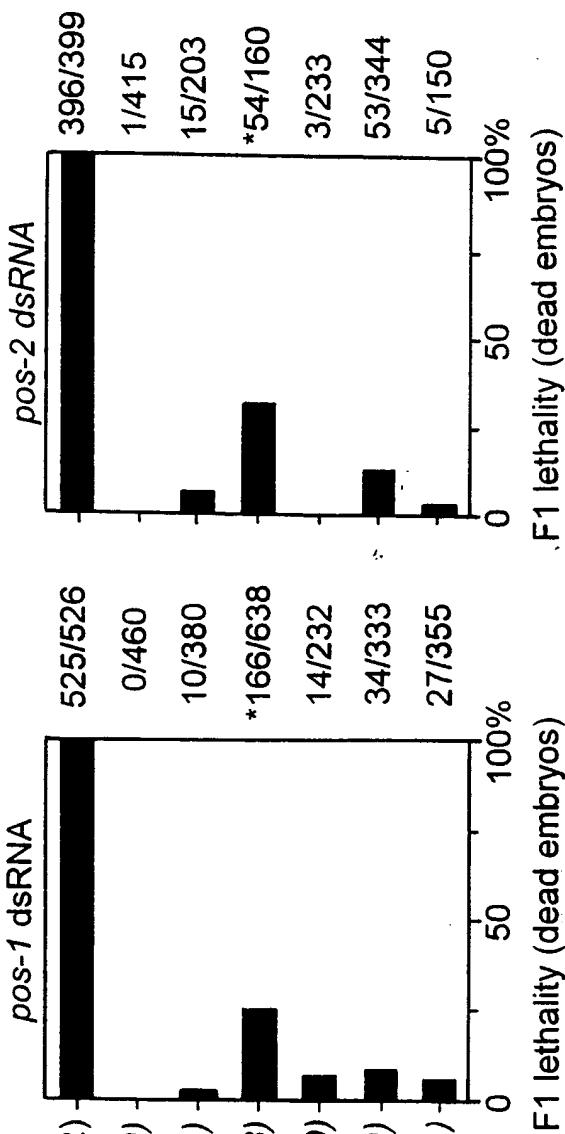


FIG. 2B

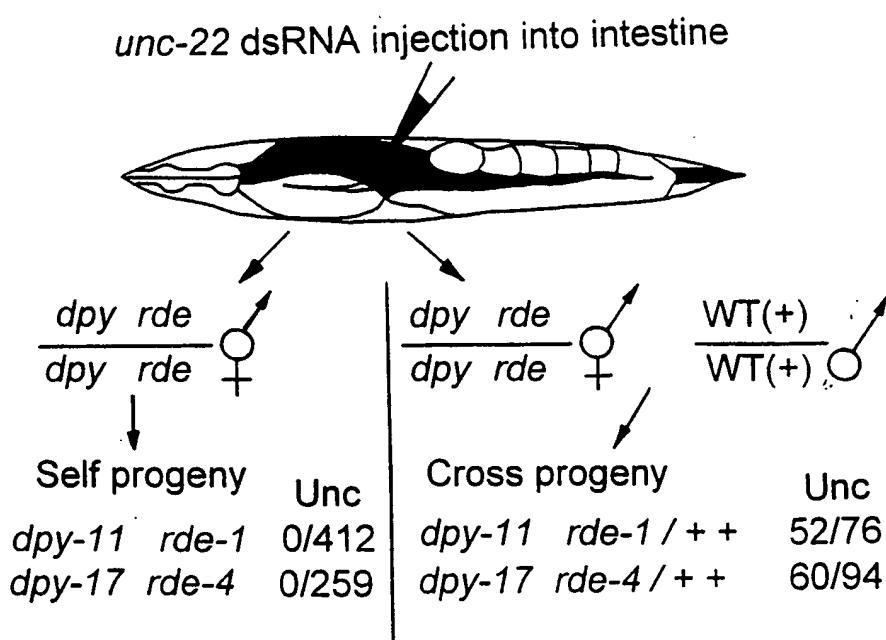


FIG. 3

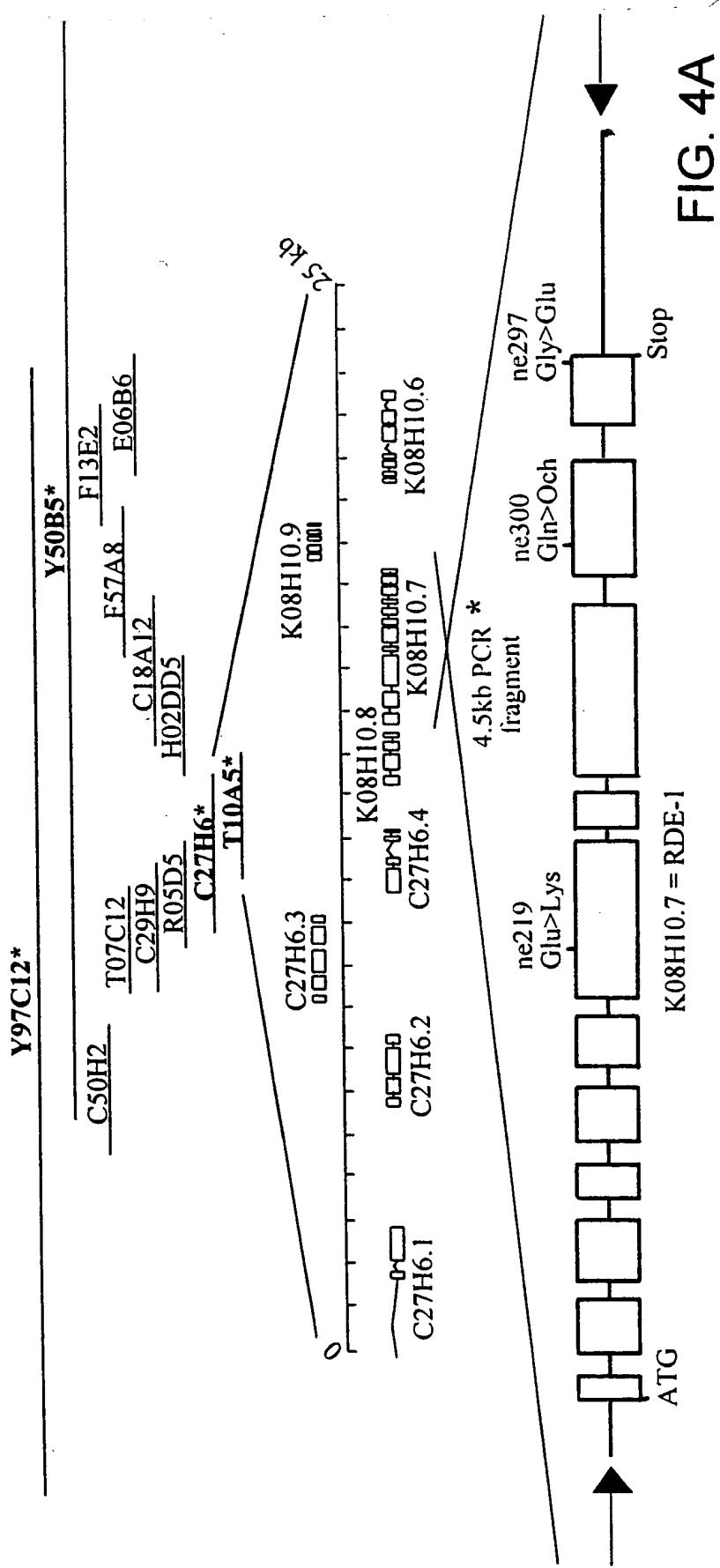


FIG. 4A

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS FOR TARGETED GENETIC INTERFERENCE

FIG. 4B-1

RDE-1	514	QINVVPEKELCCAVVVNETAGNCPLEENDVVKYTELLIGGCKFRGIRGANENRGQAQSIMYDATKNEIAYFKNCNTLNNTGIGRFEIAATE
F48F7.1	581	EGGCGTTTGGDVRVITTAATG-COHHXENDP-AEADP-CDLORYCNDACCTTIVNEECGCKAATVEVEQVEPMRPTIKONISG-----
elf2c	392	RTHGPHGCTEKKMNAAP-DRQCTEVHKSEEECLRKJDNACCEQSQCECAVACQADSYGPERHPIKNTVAG-----
ZWILLE	542	MNHKVVINGMTVSHACMF5-----KSTQENVARGEFCNELGONCEVSQMEFNPEEVIPMSAREDoveKALKVYHTSMNKTK-----
Sting	482	RTCSMFKNVHNRTVITPS-----RNLR-----EIQEFVDCIRTASSMMQN-----ICNPNEIVEIDDDRNGTYSQAIIDNAAN-----
RDE-1	604	AKNMFERLPDKEQKVEMFIISKRQLNAYGFVKHYCDHTIGVANCHITSETVTKALASLRHEKGSKRIFYQIAALKINAKLGGINQELDWS
F48F7.1	658	TOIYVWVPG-----KTPENYVPG-----VKRYKDLYVPG-----KTYQAKTAAIRTT-----GIA-----QCYQAKTAAIRTT-----
elf2c	469	TOIYVWVPG-----KTYQAKTAAIRTT-----GIA-----QCYQAKTAAIRTT-----GMA-----QCYQAKTAAIRTT-----
ZWILLE	620	GKEIEFLLLAIIEDDNGSLYGDLLKICEIDEGLI-----QCLTHV-----FISK-----QYADVLSKIN-----KGGRNTVLVDA
Sting	552	--DPOIYVVMVRSPNEEKYSCIKKRTCVDRPVP-----QVTLKVIAPRQQ-----QVTLKVIAPRQQ-----KPTGLMSIATKV-----VIQMNAKLGMAP
RDE-1	694	EIAEISPEEKERKTMPLTMYVGIDVTHPTSYSGIDYSIAAVVASINPGGT-----IIRNMIVTQECCRGERAVAHGRE-----RTDILEAKEVK
F48F7.1	725	V-----FPRTFENBYVTEGCCDIITHPPGDSRA-----SIAAVVESDAHPS-----IYAAVYVQOHRDTFTSDTY-----MVRE
elf2c	536	G-----FPRPFEOQPYVTEGCCDIITHPPGDSRA-----SIAAVVESDAHPS-----IYAAVYVQOHRDTFTSDTY-----MVRE
ZWILLE	691	IS-----CRIPLYSDIPTIIG-----IDVTHPENGEESST-----SIAAVVASOOPEVTVYAGLYCAQAHROP-----IDDLYKTTWQDPVYGTVSGGMIRD
Sting	621	W-----QVVTPLHGLWTVG-----DVCNSP-----KNNKSIYGAFAVAT-----IDQKESFRYFSTVNEHIKGQESEQMSVN-----MAC

FIG. 4B-2

INVENTOR: Craig C. Mello et al.
Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

		* ne300	
RDE-1	780	LIREFAENNDNRAPPAHIVVVYRDGVSDSEMLRVSHDELRSRSEVKOFMSERDGEDPEPKYTFIVIQKRHNTRILLRMEKDKPWNKDLTP	
F48F7.1	792	LIVOEYRNTR-EPKANIVVYRDGVSDQIENVOSELRAIRACMMLBERGYOPG---ITFIAVOKRHATRILVWVQKDQ--V	
eIF2C	603	LIGGEYKSTSR-EPKANIVVYRDGVSDQIENVOSELRAIRACMMLBERGYOPG---ITFIVOKRHATRILVWVQKDQ--V	
ZWILLE	775	ELSERARTAG-OKPLKANIVVYRDGVSDQIENVOSELRAIRACMMLBERGYOPP---VTFIVOKRHATRILVWVQKDQ--V	
Sting	687	ALRSYEQQR-SLPEREYRDGVGDQIENVOSELRAIRACMMLBERGYOPP---VTFIVOKRHATRILVWVQKDQ--V	
RDE-1	870	AETDVAVAAYKQWEEDMKESKEGETGIVNPSSGGTIVDRLIVSKYKDFELFLASHGIVLTTGDDKGMSODEVYKWTGIAFLSAR	
F48F7.1	868	-	
eIF2C	679	-	
ZWILLE	853	-	
Sting	766	-	

		E ne297	(SEQ ID NO: 13)
RDE-1	960	CRKPISLPPVHYAHLSCAKELYRTYKEHYICDYAQPRTRHEMEFLQLTNVKYPGMSEA-	(SEQ ID NO: 9)
F48F7 . 1	936	CRKSYSSPPAYAHLLVAAERARLHVDRHDSAECSHRSQSGRDLQALAVYQHQDTLRTMYTA-	(SEQ ID NO: 10)
eIF2C	747	CRKSYSSPPAYAHLLVAAERARLHVDRHDSAECSHRSQSGRDLQALAVYQHQDTLRTMYTA-	(SEQ ID NO: 6)
ZWILLE	921	CRKSYSSPPAYAHLLVAAERARLHVDRHDSAECSHRSQSGRDLQALAVYQHQDTLRTMYTA-	(SEQ ID NO: 7)
String	827	YSGTIRVPVCHYAHKLAVVAESINRAPSAGLQNLQYFL-	

FIG. 4B-3

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS FOR TARGETED GENETIC INTERFERENCE

FIG. 5A

tctgcgagttcctgaatcgttcacgtccaaacagattcgaacaatcattagaagttagcaccaagaatcgaagcatgg
tttgaatttacatttggaaatcaaagaattttcgatggtaacccgtgtcaattttgcaagtaaggttgagaaactgcga
taaaaaatcatgtgatttttgtgaagttgtcgataaactatttctacaatgcaccgaaaatgtcttctggattatctt
tccttaattgtcgccccccagtcgtgtacgtatgtacgaaaagatctaaaacaaaactgtatggcggggaaaaatgac
aatcagacaagccgcggccaagaattcgacaattttgaaaatttgaagctgaaatgcgcagaagttgggataac
aaatgttagttaaattattcaaacaattaatatacaaatttgcaggatgtcgagattgacagaacgacatctgacatt
tctagatttgcgaggaaaactcttttataaagtcaactggtaatcggacagaggaagaaatgcaaaaaaaaagtacg
atactacattgttcaaaatctatgaggaaaacaaaaagttcatttgagttccccacccatccactagtcaaagttaaaagt
ggagcaaaaagaatacgtgtaccaatggAACATCTGAAGTCACTGAGTTCCCCACCCATCCACTAGTCAGATTGATC
GGTGTGCAAGACAAGTTCTAAAGCGAGCTACACGAAAACCTCACGACTACAAAGAAAATACCCCTAAAAATGCTGAAA
AATTGGATTCTCTGAAGAGCTAAATTGGATAAGATTGGATTATGCTCCAACCTCAGATGATGCAATGTCCA
GGAAAGGTTGAAAGAGCCAATGCTGTGAATAGTGTAAATGAACAAATTGACACCAGTGATTGTTGATTCA
AGAAAAACAAATTGAATGTGGTCCCAGAAAAGAACCTTGCTGTGCTTTGTAGTCACGAAACAGCGGGAAATCCAT
GCTTAGAAGAGAACGACGTGTGAAGTGTGTTCTACGTAGATTCCGAAATATTTCAGTAAGTTCTACACCGAACT
AATTGGTGGTGCAGTTCCGTGGAAATCGAACATTGGGCCAATGAAAACAGAGGGAGCGCAATCTATTGTACGACGCGA
CGAAAAATGAATATGCCGTAAGTTCTACGAAATTGAAAGTTTAAATATCATATTACAGTTCTACAAAATTGTACAC
TAAATACCGGAATCGGTAGATTGAAATAGCCGCAACAGAAGCGAACATGTTGAACGTTCCGATAAGAAC
AAAGTCTTAATGTTCTATTATCATTCCAACGACAACGTGAATGCTACGGTTGTGAAACATTGCGATCACCCAT
CGGTGTAGCTAACGACATATTCTGAAACAGTCACAAAAGCTTGGCATCACTAAGGCACGAGAAAGGATCAAAC
GAATTTCATCAAATTGCTTGAACAGCGAAATTAGGGAGGTATTACCGAGGACTTGACTGGTCAGAAATTGCA
GAAATATCACCAGAACAGAAAAGAACACGGAAAACAATGCCATTAACATGTATGTTGAAATTGATGTAACATCCA
CTCTACAGTGGAAATTGATTCTATAGCGGTGTAGTAGCGAGTATCAATCCAGGTGGAAACTATCTATCGAAATATGA
TTGTGACTCAAGAACAGAACGCGTCCCGGTGAGCGTGCAGTGGCTATGGACGGGAAAGAACAGATAATTGGAAAGCAAA
TTCGTGAAATTGCTACAGAACATTGCGAGAACAGTGTGAGTTGCTTGAATTAAAGATCTCTGGATTTTAATTTTTG

FIG. 5B

FIG. 5C

CAGCCACAAAGTGTGAAAC- 5' UTR

1/1 31/11
ATG TCC TCG AAT TTT CCC GAA TTG GAA AAA GGA TTT TAT CGT CAT TCT CTC GAT CCG GAG
Met ser ser asn phe pro glu leu glu lys gly phe tyr arg his ser leu asp pro glu

61/21 91/31
ATG AAA TGG CTT GCG AGG CCC ACT SGT AAA TGC GAC GGC AAA TTC TAT GAG AAG AAA GTA
met lys trp leu ala arg pro thr glu lys cys asp gly lys phe tyr glu lys val

121/41 151/51
CTT CTT TTG GTA AAT TGG TTC AAG TTC TCC AGC AAA ATT TAC GAT CGG GAA TAC TAC GAG
leu leu leu val asn trp phe lys phe ser ser lys ile tyr asp arg glu tyr tyr glu

181/61 211/71
TAT GAA GTG AAA ATG ACA AAG GAA GTA TTG AAT AGA AAA CCT GGA AAA CCT TAC CCA AAA
tyr glu val lys met thr lys glu val leu asn arg lys pro gly lys pro phe pro lys

241/81 271/91
AAG ACA GAA ATT CCA ATT CCC GAT CGT GCA AAA CTC TTC TGG CAA CAT CTT CGG CAT GAG
lys thr glu ile pro ile pro asp arg ala lys leu phe trp gln his leu arg his glu

301/101 331/111
AAG AAG CAG ACA GAT TTT ATT CTC GAA GAC TAT GTT TTT GAT GAA AAG GAC ACT GTT TAT
lys lys gln thr asp phe ile leu glu asp tyr val phe asp glu lys asp thr val tyr

361/121 391/131
AGT GTT TGT CGA CTG AAC ACT GTC ACA TCA AAA ATG CTG GTT TCG GAG AAA GTA GTA AAA
ser val cys arg leu asn thr val ser lys met leu val ser glu lys val val lys

421/141 451/151
AAG GAT TCG GAG AAA AAA GAT GAA AAG GAT TTG GAG AAA AAA ATC TTA TAC ACA ATG ATA
lys asp ser glu lys asp glu lys asp leu glu lys lys ile leu tyr thr met ile

481/161 511/171
CTT ACC TAT CGT AAA AAA TTT CAC CTG AAC TTT AGT CGA GAA AAT CCG GAA AAA GAC GAA
leu thr tyr arg lys phe his leu asn phe ser arg glu asn pro glu lys asp glu

541/181 571/191
GAA GCG AAT CGG AGT TAC AAA TTC CTG AAG AAT GTT ATG ACC CAG AAA GTT CGC TAC GCG
glu ala asn arg ser tyr lys phe leu lys asn val met thr gln lys val arg tyr ala

601/201 631/211
CCT TTT GTG AAC GAG GAG ATT AAA GTA CAA TTC CGG AAA AAT TTT GTG TAC GAT AAT AAT
pro phe val asn glu glu ile lys val gln phe ala lys asn phe val tyr asp asn asn

661/221 691/231
TCA ATT CTG CGA GTT CCT GAA TCG TTT CAC GAT CCA AAC AGA TTC GAA GAA TCA TTA GAA
ser ile leu arg val pro glu ser phe his asp pro asn arg phe glu gln ser leu glu

721/241 751/251

FIG. 6A

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

CTA GCA CCA AGA ATC GAA GCA TGG TTT GGA ATT TAC ATT GGA ATC AAA GAA TTG TTC GAT
val ala pro arg ile glu ala trp phe gly ile tyr ile gly ile lys glu leu phe asp

131/261

811/271

GGT GAA CCT GTG CTC AAT TTT GCA ATT GTC GAT AAA CTA TTC TAC AAT GCA CCG AAA ATG
gly glu pro val leu asn phe ala ile val asp lys leu phe tyr asn ala pro lys met

341/281

871/291

TCT CTT CTG GAT TAT CTT CTC CTA ATT GTC GAC CCC CAG TCG TGT AAC GAT GAT GTA CGA
ser leu leu asp tyr leu leu ile val asp pro gin ser cys asn asp asp val arg

901/301

931/311

AAA GAT CTT AAA ACA AAA CTG ATG GCG GGA AAA ATG ACA ATC AGA CAA GCC GCG CGG CCA
lys asp leu lys thr lys leu met ala gly lys met thr ile arg gln ala ala arg pro

961/321

991/331

AGA ATT CGA CAA TTA TTG GAA AAT TTG AAG CTG AAA TGC GCA GAA GTT TGG GAT AAC GAA
arg ile arg gln leu leu glu asn leu lys leu lys cys ala glu val trp asp asn glu

1021/341

1051/351

ATG TCG AGA TTG ACA GAA CGA CAT CTG ACA TTT CTA GAT TTG TGC GAG GAA AAC TCT CTT
met ser arg leu thr glu arg his leu thr phe leu asp leu cys glu glu asn ser leu

1081/361

1111/371

GTT TAT AAA GTC ACT GGT AAA TCG GAC AGA GGA AGA AAT GCA AAA AAG TAC GAT ACT ACA
val tyr lys val thr gly lys ser asp arg gly arg asn ala lys lys tyr asp thr thr

1141/381

1171/391

TTG TTC AAA ATC TAT GAG GAA AAC AAA AAG TTC ATT GAG TTT CCC CAC CTA CCA CTA GTC
leu phe lys ile tyr glu glu asn lys phe ile glu phe pro his leu pro leu val

1201/401

1231/411

AAA GTT AAA AGT GGA GCA AAA GAA TAC GCT GTA CCA ATG GAA CAT CTT GAA GTT CAT GAG
lys val lys ser gly ala lys glu tyr ala val pro met glu his leu glu val his glu

1261/421

1291/431

AGG CCA CAA AGA TAC AAG AAT CGA ATT GAT CTG GTG ATG CAA GAC AAG TTT CTA AAG CGA
lys pro gln arg tyr lys asn arg ile asp leu val met gln asp lys phe leu lys arg

1321/441

1351/451

GCT ACA CGA AAA CCT CAC GAC TAC AAA GAA AAT ACC CTA AAA ATG CTG AAA GAA TTG GAT
ala thr arg lys pro his asp tyr lys glu asn thr leu lys met leu lys glu leu asp

1381/461

1411/471

TTC TCT TCT GAA GAG CTA AAT TTT GTT GAA AGA TTT GGA TTA TGC TCC AAA CTT CAG ATG
phe ser ser glu glu leu asn phe val glu arg phe gly leu cys ser lys leu gln met

1441/481

1471/491

ATC GAA TGT CCA GGA AAG GTT TTG AAA GAG CCA ATG CTT GTG AAT AGT GTA AAT GAA CAA
ile glu cys pro gly lys val leu lys glu pro met leu val asn ser val asn glu gln

1501/501

1531/511

ATT AAA ATG ACA CCA GTG ATT CGT GGA TTT CAA GAA AAA CAA TTG AAT GTG GTT CCC GAA
ile lys met thr pro val ile arg gly phe gln glu lys gln leu asn val val pro glu

FIG. 6B

1661/521 1691/531
AAA GAA CTT TGC TGT GCT GTT CTT GTC AAC GAA ACA GCG GGA AAT CCA TGC TTA GAA
lys glu leu cys cys ala val phe val val asn glu thr ala gly asn pro cys leu glu

1621/541 1651/551
GAG AAC GAC GTT GTT AAG TTC TAC ACC GAA CTA ATT GGT GGT TGC AAG TTC CGT GGA ATA
glu asn asp val val lys phe tyr thr glu leu ile gly gly cys lys phe arg gly ile

1681/561 1711/571
CCA ATT GGT GCC AAT GAA AAC AGA GGA GCG CAA TCT ATT ATG TAC GAC GCG ACG AAA AAT
arg ile gly ala asn glu asn arg gly ala gin ser ile met tyr asp ala thr lys asn

1741/581 1771/591
GAA TAT GCC TTC TAC AAA AAT TGT ACA CTA AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC
glu tyr ala phe tyr lys asn cys thr leu asn thr gly ile gly arg phe glu ile ala

1801/601 1831/611
GCA ACA GAA GCG AAG AAT ATG TTT GAA CGT CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG
ala thr glu ala lys asn met phe glu arg leu pro asp lys glu gin lys val leu met

1861/621 1891/631
TTC ATT ATC ATT TCC AAA CCA CAA CTG AAT GCT TAC GGT TTT GTG AAA CAT TAT TGC GAT
phe ile ile ile ser lys arg gin leu asn ala tyr gly phe val lys his tyr cys asp

1921/641 1951/651
CAC ACC ATC GGT GTA GCT AAT CAG CAT ATT ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA
his thr ile gly val ala asn gin his ile thr ser glu thr val thr lys ala leu ala

1981/661 2011/671
TCA CTA AGG CAC GAG AAA GGA TCA AAA CGA ATT TTC TAT CAA ATT GCA TTG AAA ATC AAC
ser leu arg his glu lys gly ser lys arg ile phe tyr gin ile ala leu lys ile asn

2041/681 2071/691
GCG AAA TTA GGA GGT ATT AAC CAG GAG CTT GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA
ala lys leu gly gly ile asn gin glu leu asp trp ser glu ile ala glu ile ser pro

2101/701 2131/711
GAA GAA AAA GAA AGA CGG AAA ACA ATG CCA TTA ACT ATG TAT GTT GGA ATT GAT GTA ACT
glu glu lys glu arg arg lys thr met pro leu thr met tyr val gly ile asp val thr

2161/721 2191/731
CAT CCA ACC TCC TAC AGT GGA ATT GAT TAT TCT ATA GCG GCT GTA GTA GCG AGT ATC AAT
his pro thr ser tyr ser gly ile asp tyr ser ile ala ala val val ala ser ile asn

2221/741 2251/751
CCA GGT GGA ACT ATC TAT CGA AAT ATG ATT GTG ACT CAA GAA GAA TGT CGT CCC GGT GAG
pro gly gly thr ile tyr arg asn met ile val thr gin glu glu cys arg pro gly glu

2281/761 2311/771
CGT GCA GTG GCT CAT CGA CGG GAA AGA ACA GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG
arg ala val ala his gly arg glu arg thr asp ile leu glu ala lys phe val lys leu

2341/781 2371/791
CTC AGA GAA TTC GCA GAA AAC AAC GAC AAT CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA
leu arg glu phe ala glu asn asn asp asn arg ala pro ala his ile val val tyr arg

2401/801 2431/811
GAC GGA GTT AGC GAT TCG GAG ATG CTA CGT GTT AGT CAT GAT GAG CTT CGA TCT TTA AAA
asp gly val ser asp ser glu met leu arg val ser his asp glu leu arg ser leu lys

2461/821 2491/831
AGC GAA GTA AAA CAA TTC ATG TCG GAA CGG GAT GGA GAA GAT CCA GAG CCG AAG TAC ACG
ser glu val lys gin phe met ser glu arg asp gly glu asp pro glu pro lys tyr thr
2521/841 2551/851
TTC ATT GTG ATT CAG AAA AGA CAC AAT ACA CGA TTG CTT CGA AGA ATG GAA AAA GAT AAG
phe ile val ile gin lys arg his asn thr arg leu leu arg arg met glu lys asp lys

2581/861 2611/871
CCA GTG GTC AAT AAA GAT CTT ACT CCT GCT GAA ACA GAT GTC GCT GTT GCT GCT GTT AAA
pro val val asn lys asp leu thr pro ala glu thr asp val ala val ala val lys

2641/881 2671/891
CAA TGG GAG GAG GAT ATG AAA GAA AGC AAA GAA ACT GGA ATT GTG AAC CCA TCA TCC GGA
gln trp glu glu asp met lys glu ser lys glu thr gly ile val asn pro ser ser gly

2701/901 2731/911
ACA ACT GTG GAT AAA CTT ATC GTT TCG AAA TAC AAA TTC GAT TTT TTC TTG GCA TCT CAT
thr thr val asp lys leu ile val ser lys tyr lys phe asp phe leu ala ser his

2761/921 2791/931
CAT GGT GTC CTT GGT ACA TCT CGT CCA GGA CAT TAC ACT GTT ATG TAT GAC GAT AAA GGA
his gly val leu gly thr ser arg pro gly his tyr thr val met tyr asp asp lys gly

2821/941 2851/951
ATG AGC CAA GAT GAA GTC TAT AAA ATG ACC TAC GGA CTT GCT TTT CTC TCT GCT AGA TGT
met ser gln asp glu val tyr lys met thr tyr gly leu ala phe leu ser ala arg cys

2881/961 2911/971
CGA AAA CCC ATC TCG TTG CCT GTT CCG GTT CAT TAT GCT CAT TTA TCA TGT GAA AAA GCG
arg lys pro ile ser leu pro val pro val his tyr ala his leu ser cys glu lys ala

2941/981 2971/991
AAA GAG CTT TAT CGA ACT TAC AAG GAA CAT TAC ATC GGT GAC TAT GCA CAG CCA CGG ACT
lys glu leu tyr arg thr tyr lys glu his tyr ile gly asp tyr ala gln pro arg thr

3001/1001 3031/1011
CGA CAC GAA ATG GAA CAT TTT CTC CAA ACT AAC GTG AAG TAC CCT GGA ATG TCG TTC GCA
arg his glu met glu his phe leu gln thr asn val lys tyr pro gly met ser phe ala

3061/1021 3091/1031
TAA CAT TTT GCA AAA GTG TCG CCC GTT TCA ATC AAA TTT TTC AAT TGT AGA TAT TGT ACT
CCH (SEQ ID NO:3)

3121/1041 3151/1051
TAC TTT TTT TTA AAG CCC GGT TTC AAA AAT TCA TTC CAT GAC TAA CGT TTT CAT AAA TTA

3181/1061
CTT GAA ATT TAA AAA AAA AAA AAA (SEQ ID NO:2)

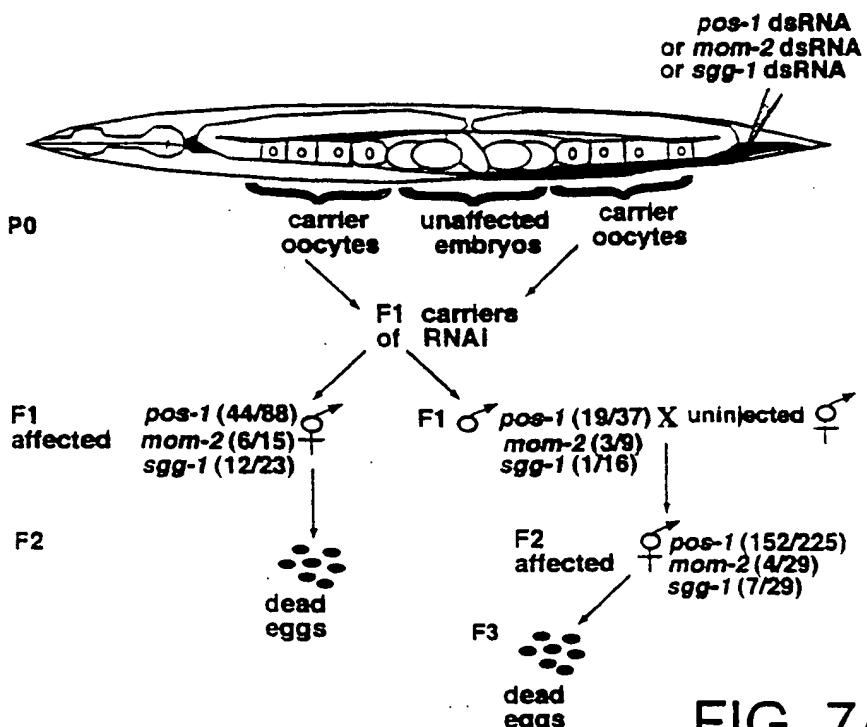
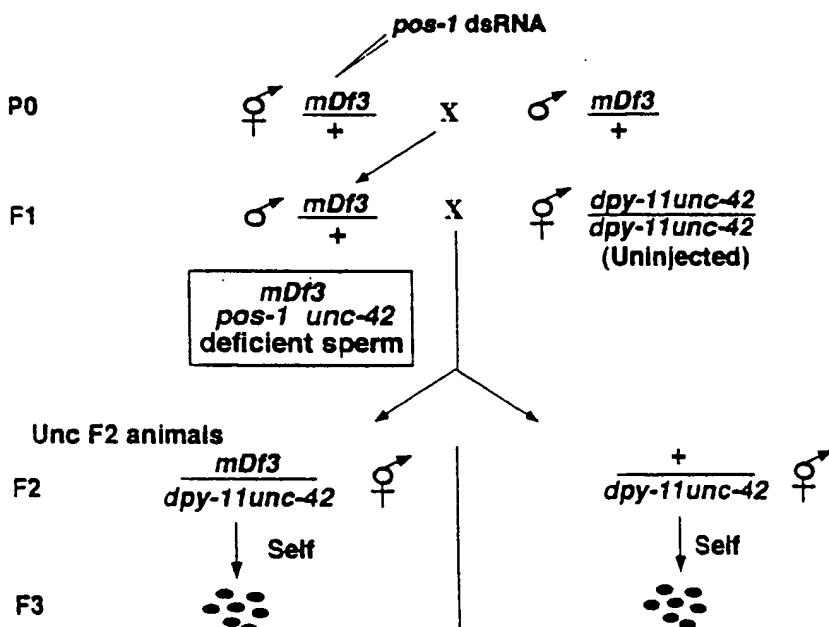


FIG. 7A



Results:

6/9 $mDf3$ sperm gave rise to F2 with 100% ($n > 1000$) F3 pos-1 embryos.

3/27 (+) sperm gave rise to F2 with 100% ($n > 500$) F3 pos-1 embryos.

FIG. 7B

Injected P0		F1	
	<u>rde-1 unc-42</u> + <i>pos-1</i> dsRNA	$\xrightarrow{\text{self X}}$	<i>rde-1 (-)</i> 11/24 <i>rde-1 (+)</i> 9/72
	<u>rde-2 unc-13</u> + <i>pos-1</i> dsRNA	\longrightarrow	<i>rde-2 (-)</i> 0/39 <i>rde-2 (+)</i> 23/78
	<u>mut-7 dpy-17</u> + <i>pos-1</i> dsRNA	\longrightarrow	<i>mut-7 (-)</i> 0/15 <i>mut-7 (+)</i> 20/50
	<u>rde-4 unc-69</u> + <i>pos-1</i> dsRNA	\longrightarrow	<i>rde-4 (-)</i> 5/15 <i>rde-4 (+)</i> 11/48

FIG. 8A

P0	Injected F1
	<u>rde-1 unc-42</u> + <i>pos-1</i> dsRNA
	<u>rde-4 unc-69</u> + <i>pos-1</i> dsRNA

FIG. 8B

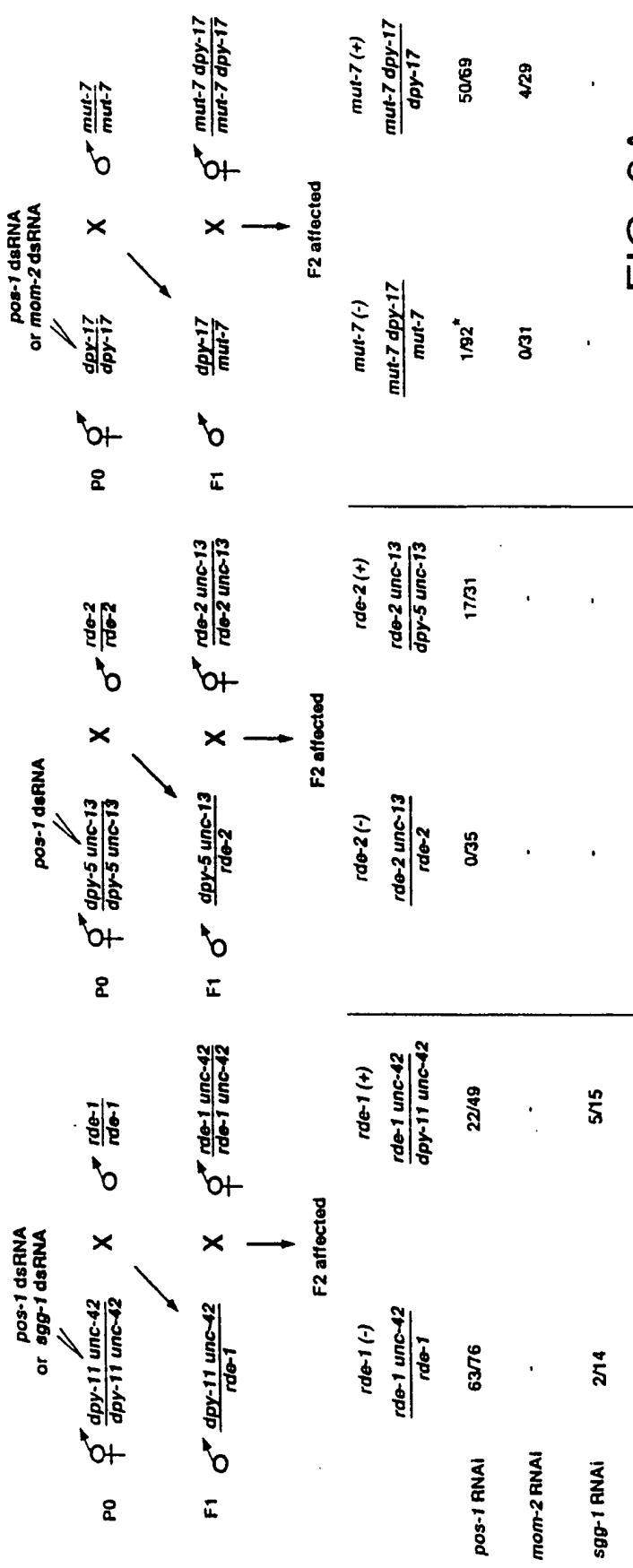


FIG. 9A

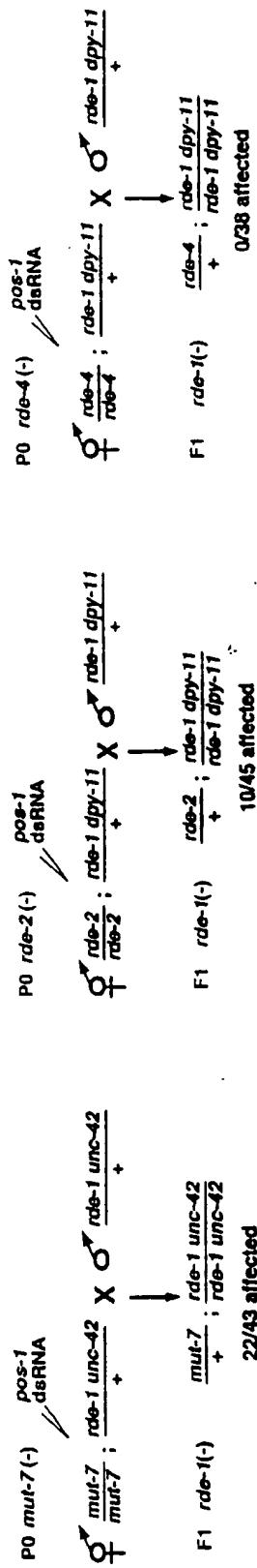


FIG. 9B

10 20 30 40 50 60
ATGGATTAAACCAACTAACGTTGAAAGCGTTTCGGTGGATCAGATGTTCTATGAAG
M D L T K L T F E S V F G G S D V P M K

70 80 90 100 110 120
CCTTCCCGATCGGAGGATAACAAAACGCCAAGAACAGAACAGATTTGGAGATGTTCTG
P S R S E D N K T P R N R T D L E M F L

130 140 150 160 170 180
AAGAAAAACTCCCTCATGGTACTAGAACAGGCTGCTAAGGCTGTCTATCAAAGACGCCA
K K T P L M V L E E A A K A V Y Q K T P

190 200 210 220 230 240
ACTTGGGGCACTGTCGAACCTCCTGAAGGCTTCGAGATGACGTTGATTCTGAATGAAATT
T W G T V E L P E G F E M T L I L N E I

250 260 270 280 290 300
ACTGTAAAAGGCCAGGCAACAAGCAAGAACAGCTGGAGACAAAAGGCTGCTGTTGAATAT
T V K G Q A T S K K A A R Q K A A V E Y

310 320 330 340 350 360
TTACGCAAGGTTGGAGAAAGGAAAGCACGAAATCTTCTCATTCCTGAAACAACAAA
L R K V V E K G K H E I F F I P G T T K

370 380 390 400 410 420
GAAGAAGCTCTTCAAAATATTGATCAAATATCGGATAAGGCTGAGGAATTGAAACGATCA
E E A L S N I D Q I S D K A E E L K R S

430 440 450 460 470 480
ACTTCAGATGCTGTTCAAGGATAACGATAACGATGATTCGATTCTACAAAGTGCTGAATT
T S D A V Q D N D N D D S I P T S A E F

490 500 510 520 530 540
CCACCTGGTATTCGCCAACCGAGAATTGGTCGAAAGTTGAGGAAAAATCTCAAAAA
P P G I S P T E N W V G K L Q E K S Q K

550 560 570 580 590 600
AGCAAGCTGCAAGCCCCAATCTATGAAGATTCCAAGAACGAGAGAACCGAGCGTTCTTG
S K L Q A P I Y E D S K N E R T E R F L

610 620 630 640 650 660
GTTATATGCACGATGTCAATCAAAAAACCAAGAGGAATCAGAAGTAAGAACAGGACGCA
V I C T M C N Q K T R G I R S K K K D A

670 680 690 700 710 720
AAGAACATCTGCAGCATGGTGTGAAAGCGTTGGAAAGACGGTATCGAATCTCTGGAA
K N L A A W L M W K A L E D G I E S L E

730 740 750 760 770 780
TCATATGATATGGTGTGATTGAAAGAACGCTGAACATTACTCGAAATT
S Y D M V D V I E N L E E A E H L L E I

FIG. 10A

790	800	810	820	830	840
CAGGATCAAGCATCCAAGATTAAAGACAAGCATTCCGCACTGATTGATATACTCTCGGAC					
Q	D	Q	A	S	K
I	K	D	K	H	S
A	L	I	D	I	L
S	D	I	L	S	D
850	860	870	880	890	900
AAGAAAAGATTTCAGACTACAGCATGGATTCAACGTATTATCAGTGAGCACAAATGGGA					
K	K	R	F	S	D
Y	S	M	D	F	N
V	L	S	V	S	T
L	S	V	S	T	M
910	920	930	940	950	960
ATACATCAGGTGCTATTGAAATCTCGTCCGGCGCTAGTTCTCCAGACCCGACGAT					
I	H	Q	V	L	E
Q	V	L	E	I	S
L	E	I	S	F	R
E	I	S	F	R	R
970	980	990	1000	1010	1020
TTGGAAATGGGAGCAGAACACACCCAGACTGAAGAAAATTATGAAGGCTACTGCCGAGAAG					
L	E	M	G	A	E
E	H	T	Q	T	E
H	T	Q	T	E	E
T	Q	T	E	E	I
1030	1040	1050	1060	1070	1080
GAAAAGCTACGGAAGAAGAACATGCCAGATTCCGGGCCGCTAGTGTGCTGGACATGGT					
E	K	L	R	K	K
N	M	P	D	S	G
M	P	D	S	G	P
N	P	D	S	G	L
1090	1100	1110	1120	1130	1140
TCATCGCGGAAGAGGGCTAACACAGTGTGCTTGTAAATCGGCATTATCCATTCAACACC					
S	S	A	E	E	A
A	E	E	A	K	Q
E	A	K	Q	C	A
A	K	Q	C	A	C
K	Q	C	A	K	K
1150	1160	1170	1180	1190	1200
TATGATTTACGGATTGAAAATATTATTGCGTATTCTGAAAAATGAAGCGTCTGAATGA					
Y	D	F	T	D	*
*	K	Y	Y	C	V
K	K	K	K	F	L
K	K	K	K	L	K
K	K	K	K	N	E
K	K	K	K	E	A
K	K	K	K	S	E
K	K	K	K	A	*
1210	1220	1230	(SEQ ID NO:4)		
L	*	K	K	K	(SEQ ID NO:5)
K	K	K	K	K	

FIG. 10B

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FOR TARGETED GENETIC INTERFERENCE

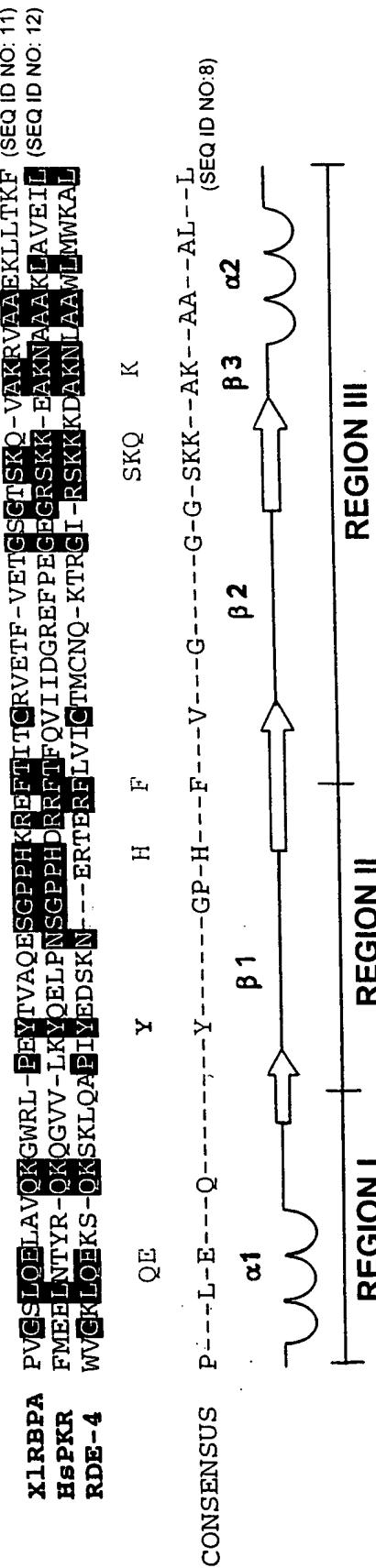
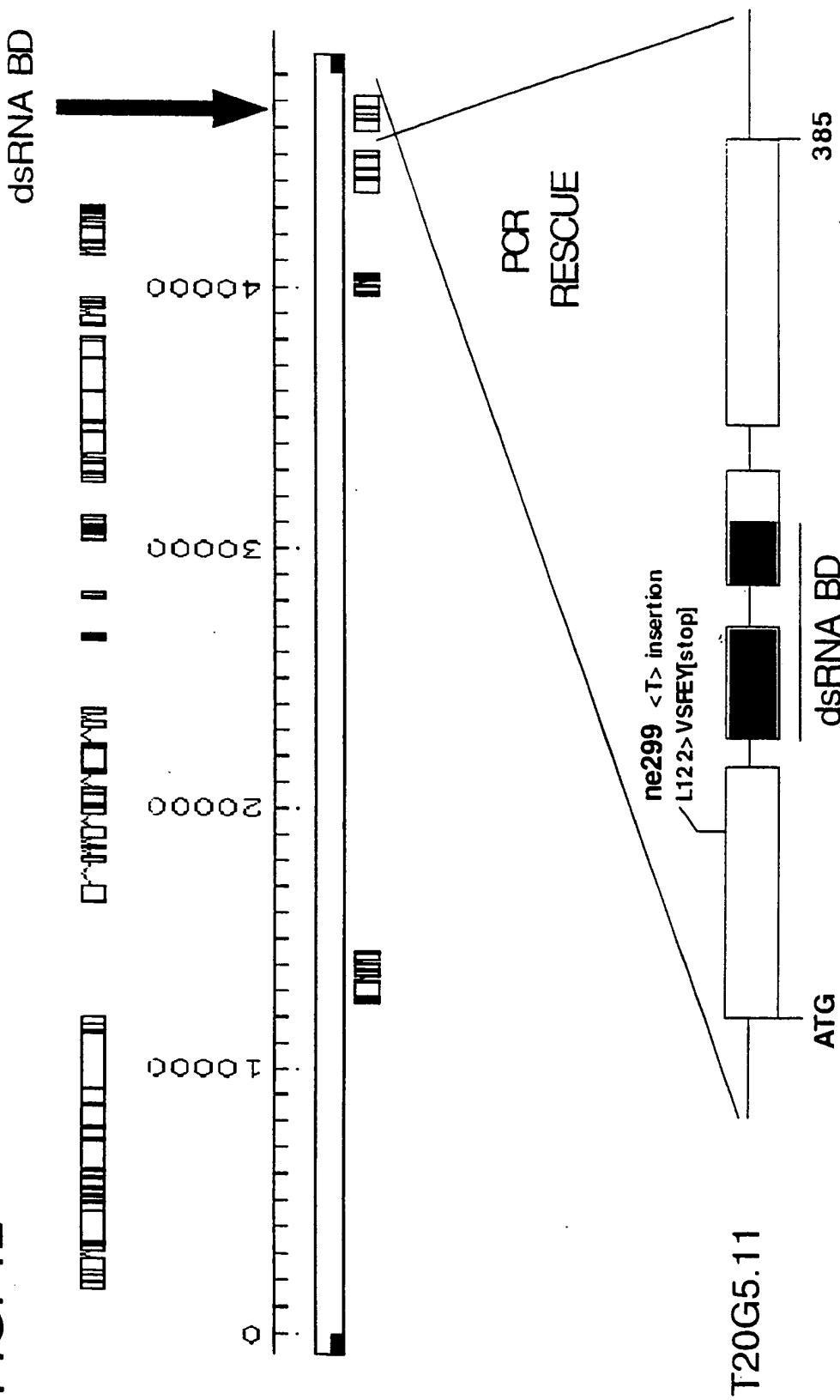


FIG. 11

FIG. 12
Rescue of *rde-4*:



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